The same DNA answer:
everything everywhere all at once

Mid-Atlantic Association of Forensic Scientists

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Cybergenetics

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Physical laws are **the same**
for everything, everywhere, all at once

$F = ma$

$F = ma$

$F = ma$

Gravity
Motion
Force
Electricity
Magnetism
Light
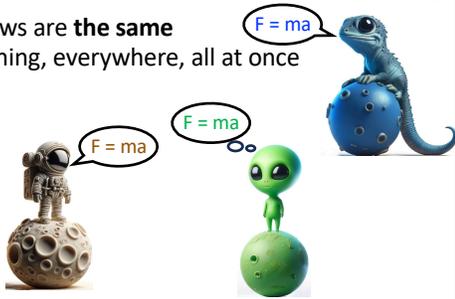
What about the laws of forensic DNA science?

Genotype
Mixture weight
Likelihood ratio
Probability
Inclusion
Exclusion

Protocol differences: sample

Touch DNA?
Damaged DNA?
Too little DNA?
Complex mixtures?
DNA is too old?
Related people?

Data differences: laboratory

Extraction
STR kit
Sequencer
EPG, NGS
Reporting
Error rate

Interpretation differences: method

Manually
Thresholds
Calibration
Parameters
Stutter
Computation

People differences: analyst

Education
Training
Experience
Knowledge
Systems
Preferences

Outcome differences: reporting

Inclusion/Exclusion
Match statistics
Likelihood ratio
"Uninformative"
"Inconclusive"
"No comparison"

Community differences: different answers

MIX13 Case 5 Outcomes with Suspect C
(whose genotypes were not present in the mixture)

Some Differences in Reporting Statistics

Lab ID	Kits Used	Caucasians	African Americans	Hispanics
90	ProPlus/Cofiler	1.10E+15	2.13E+14	3.09E+16
34	ProPlus/Cofiler	2.40E+11	7.00E+09	9.80E+10
33	ProPlus/Cofiler	2.94E+08	1.12E+08	1.74E+09
6	ProPlus/Cofiler	40,000,000	3,500,000	280,000,000
9	ProPlus/Cofiler	1.14E+07	1.97E+07	1.54E+08
79	ProPlus/Cofiler	930,000	47,900	1,350,000
16	ProPlus/Cofiler	434,600	31,710	399,100

Remember that these labs are interpreting the same MIX05 electropherograms

Variation in assessments of suitability and number of contributors for DNA mixtures

Consequences of differences: multiverse

Same data, different answer
Match vs. not match
Include vs. exclude
Implicate suspect
Exonerate suspect
Silence: no answer at all

d = Gw

TrueAllele laws are **the same**
for everything, everywhere, all at once

d = Gw

Genotype
Mixture weight
Likelihood ratio
d = Gw
Probability
Implicate
Exonerate
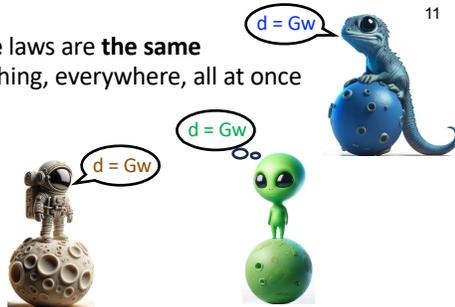
How TrueAllele works

- No lab calibration – learns from DNA data
- Bayesian inference – uses all the data
- No thresholds or other parameters
- Explains data peak patterns
- Separates contributor genotypes
- Gives accurate likelihood ratios
- No limits – up to ten contributors
- "It's like using a calculator"

TrueAllele® Proficiency study

- Goal was to show that trained analysts were proficient in TrueAllele
- Secondary goal was to examine differences in TrueAllele laboratories
  - 10 participating TrueAllele laboratories
  - 32 TrueAllele trained analysts

TrueAllele Proficiency study design

- Multiple TrueAllele labs submitted a mixture sample
  - created in their lab
  - representative data
  - some samples from adjudicated cases
- Also provided a matching reference profile
- Sample and reference anonymized
- Analysts from labs signed up to participate in study

TrueAllele Proficiency study protocol

- Cybergenetics provided each study participant with each of the 10 mixture data samples
- Each participating analyst processed each mixture sample
- Once all processing completed, references sent out for comparison
  - Analysts did not have reference samples when processing the mixture data
  - References were not needed for evidence interpretation
- Returning results shows that the analyst is proficient in TrueAllele

Mixture samples: STR kits used

Kit	sample
Applied Biosystems™ Globalfiler	4
Promega PowerPlex® 16	1
Promega PowerPlex® Fusion 5C	3
Promega PowerPlex® Fusion 6C	1
Qiagen Investigator® 24plex GO!	1

Mixture samples: DNA sequencers used

Sequencer	sample
ABI310	1
ABI3130xl	2
ABI3500	5
ABI3500xl	2

Mixture samples: number of contributors

DNA contributors	sample
three	2
four	7
five	1

Analyst: task 1

- Create 'request' for each mixture sample in triplicate
  - A request is a computer run
  - Replicates show reproducibility
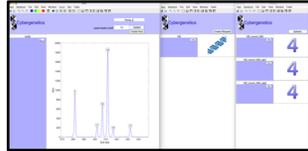
Analyst: task 2

- Use TrueAllele to compare evidence with references
  - Determine matching reference
  - Provide match statistics for each replicate
  - Each analyst returns a total of 30 match statistics
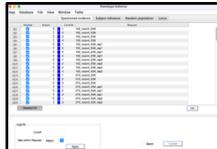
Results: across 8 **cases**
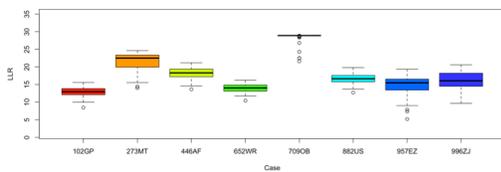
Results: across 10 **laboratories**

Case 102GP
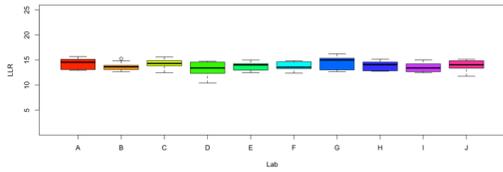
Results: laboratory

- ANOVA (ANalysis Of VAriance)
  - Degrees of Freedom: 9
  - Sum of Squares: 3
  - Mean Square: 4.2
  - F-statistic: 1.231
  - p-value: **0.273** > 0.05

Any way
Anywhere
Any time

Across all the cases

Results: across 32 **analysts**

Case 102GP
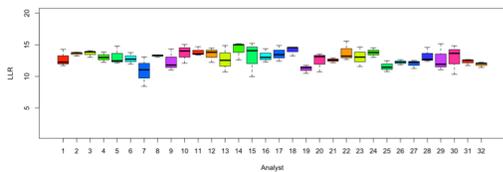
Results: analyst

- ANOVA
  - Degrees of Freedom: 31
  - Sum of Squares: 79
  - Mean Square: 2.6
  - F-statistic: 0.732
  - p-value: **0.856** > 0.05

Any one

Across all the cases

Study conclusions

- Laboratories
  - ~~STR kit~~
  - ~~Sequencer~~
  - ~~Reporting~~
  - ~~Thresholds~~
  - ~~Calibration~~
  - ~~Parameters~~
  - ~~Stutter~~
  - ~~Computation~~
  - same DNA result

- Analysts
  - ~~Education~~
  - ~~Training~~
  - ~~Experience~~
  - ~~Knowledge~~
  - same DNA result

Significance: Everything everywhere all at once

- The same DNA answer – any way, anywhere, any time, anyone
- One validation study applies to all
  - Any validated kit, sequencer, or method
- Same reliability applies to all
  - Trained analysts get the same result
- Can process legacy cases
- Even opposing experts will get the same DNA answer

More information

http://www.cybgen.com/information
- Courses
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http://www.youtube.com/user/TrueAllele
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